AMENDMENTS TO THE CLAIMS

Please amend the claims as indicated hereafter.

Claims:

1. (Withdrawn) A system for assaying multiple nucleic acid molecules in one or more biological samples having one or more nucleic acid targets per sample comprising:

a plurality of nucleic acid proves, wherein each nucleic acid of the plurality is different from other nucleic acids in the plurality, and

a plurality of intermediary nucleic acids, wherein each intermediary nucleic acid comprises a first region and a second region, wherein each intermediary nucleic acid is different from other intermediary nucleic acids in the plurality of intermediary nucleic acids by comprising a different first region, wherein the first region of each intermediary nucleic acid is complementary to a different nucleic acid probe of the plurality of nucleic acid probes, and wherein the second region of each intermediary nucleic acid is complementary to a potential target nucleic acid in a sample, wherein each probe of the plurality of nucleic acid probes and each second region of each intermediary nucleic acid comprises unstructured nucleotides, such that the second region of each intermediary nucleic acid has a reduced ability to form a stable duplex with a nucleic acid probe having regions of complementarity, wherein the second region of each intermediary nucleic acid forms a stable duplex with a complementary target nucleic acid, and wherein each nucleic acid probe forms a stable duplex with a complementary first region of an intermediary nucleic acid.

2. (Withdrawn) The system of claim 1, wherein the nucleic acid probes comprising modified and unmodified nucleotides and the second region of intermediary nucleic acids comprising modified nucleotides comprise complementary nucleotides that have a reduced ability to form base pairs with each other, wherein the modified nucleotides form base pairs with unmodified nucleotides.

3. (Withdrawn) The system of claim 1, wherein the modified nucleotides comprise A' and T' wherein A' and T' have a reduced ability to form a base pair, wherein A' forms a base pair with T*, and wherein T' forms a base pair with A*.

4. (Withdrawn) The system of claim 3, wherein A' is 2-aminoadenosine, wherein T is 2-thiothymidine, wherein A* is adenosine and wherein T* is thymidine.

5. (Withdrawn) The system of claim 1, wherein the modified nucleotides comprise G' and C' wherein G' and C' have a reduced ability to form a base pair, wherein G' forms a base pair with C*, and wherein C' forms a base pair with G*.

6. (Withdrawn) The system of claim 3, wherein G' is inosine, wherein C' is pyrrolopyrimidine, wherein G* is guanosine and wherein C* is cytosine.

7. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe corresponds to a known location in the array pattern.

8. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe associated with a known bead particle.

9. (Withdrawn) The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe is associated with a defined tag moiety wherein the tag is detectable by mass electrophoretic mobility or optical property.

10. (Currently amended) A method of assaying target nucleic acid molecules by tagging and sorting the target molecules, comprising the steps of:

a) providing a first plurality of nucleic acids, wherein each nucleic acid of the first plurality is different from other nucleic acids in the first plurality, and wherein the first plurality of nucleic acids are immobilized on a surface;

b) providing a second plurality of nucleic acids, wherein each second nucleic acid of the second plurality comprises a first region and a second region, wherein each first region of each second nucleic acid has a different sequence from other first regions of other nucleic acids in the second plurality, wherein the first region of each second nucleic acid is complementary to a different first nucleic acid of the first plurality, wherein at least one second region of the second nucleic acids in the second plurality is complementary to a target nucleic acid in a biological sample[[s]], wherein each ~~first~~ nucleic acid of the first plurality and each second region of each second nucleic acid of the second plurality comprise unstructured nucleotides such that the second region of each second nucleic acid has a reduced ability to hybridize to a first ~~probe~~ nucleic acid of the first plurality having a

complementary sequence without reducing the ability of the second region of each second nucleic acid to hybridize to a complementary nucleic acid molecule in a biological sample;

c) providing a biological sample containing nucleic acids to be analyzed;

d) contacting the biological sample with the second plurality of ~~probes~~ nucleic acids under conditions that permit hybridization of complementary sequences between the nucleic acid molecules in the sample and the second region of a second nucleic acids of the second plurality;

e) contacting the second plurality of ~~probes~~ nucleic acids with the first plurality of ~~probes~~ nucleic acids under conditions that permit hybridization of complementary sequences between the first region of a second ~~probe~~ nucleic acid of the second plurality and the first ~~probes~~ nucleic acids in the first plurality~~;~~;

f) detecting nucleic acids in the biological sample that have hybridized to a nucleic acid of the second plurality by detecting a signal of a label that is part of the nucleic acids chosen from at least one of: the biological sample and the second plurality of nucleic acids;

g) determining a position on the substrate of the detectable signal of the label; and

~~g~~ h) determining the sequence of the nucleic acid in the biological sample that has hybridized to a nucleic acid of the second plurality by correlating the position of the signal to the sequence.

11. (Original) The method of claim 10, wherein the steps of (d) and (e) are performed simultaneously.

12. (Original) The method of claim 10, wherein after step (e), unhybridized nucleic acids are removed.

13. (Currently amended) The method of claim 10, wherein the step of detecting the label further comprises detecting the label by measuring light emission from the label.

14. (Currently amended) The method of claim 10, wherein the step of contacting the biological sample with the second plurality of ~~probes~~ nucleic acids further comprises labeling the ~~probes~~ nucleic acids that having hybridized with a nucleic acid in the sample with a detectable label.

15-16. (Cancelled)

17. (Newly added) A method of assaying target nucleic acid molecules by tagging and sorting the target molecules, comprising the steps of:

hybridizing a first plurality of nucleic acids on an array, wherein each of the first plurality of nucleic acids is difference from the other nucleic acids in the first plurality;

hybridizing a second plurality of nucleic acids to the first plurality of nucleic acids at a first region on each of the nucleic acids of the second plurality;

hybridizing at least one of the nucleic acids in the second plurality of nucleic acids to a complementary target nucleic acid in a biological sample at a second region on the nucleic acid of the second plurality,

wherein each nucleic acid of the first plurality and each second region of each nucleic acid of the second plurality comprise unstructured nucleotides such that the second region of each second nucleic acid has a reduced ability to hybridize to the nucleic acids of the first plurality, without reducing the ability of the second region of each second nucleic acid to hybridize to the target nucleic acid in the biological sample;

including a label on at least one of the nucleic acids chosen from the second plurality of nucleic acids and the target nucleic acid in the biological sample;

detecting the target nucleic acid in the biological sample that have hybridized to a nucleic acid of the second plurality by detecting a signal from the label;

determining a position on the array of the detectable signal of the label; and

determining the sequence of the target nucleic acid in the biological sample that has hybridized to a nucleic acid of the second plurality by correlating the position of the signal on the array to the sequence of the nucleic acid to which the target nucleic acid is hybridized.

18. (Newly added) The method of claim 17, wherein the step of detecting the signal from the label further comprises detecting the signal from the label by measuring light emission from the label.